Package: DSBayes (via r-universe)

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Type Package

Title Bayesian Subgroup Analysis in Clinical Trials

Description Calculate posterior modes and credible intervals of parameters of the Dixon-Simon model for subgroup analysis (with binary covariates) in clinical trials. For details of the methodology, please refer to D.O. Dixon and R. Simon (1991), Biometrics, 47: 871-881.

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Imports BB

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DSBayes-package *Bayesian subgroup analysis in clinical trials*

Description

Calculate posterior modes and credible intervals of parameters of the Dixon-Simon model for subgroup analysis (with binary covariates) in clinical trials.

Details

Package:	DSBayes
Version:	1.1
Date:	Dec 27, 2013
Depends:	R (>= 2.15.1)
Imports:	BB
License:	GPL Version 2

The main functions in this package are:

```
DSBayes: A function to calculate the posterior mode and credible interval of the parameters in the Dixon
```

Author(s)

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References

Dixon D. and Simon R. (1991). Bayesian Subset Analysis. *Biometrics*, 47, 871-881

DSBayes *Bayesian subgroup analysis in clinical trials*

Description

Calculate posterior modes and credible intervals of parameters of the Dixon-Simon model for subgroup analysis (with binary covariates) in clinical trials.

Usage

```
DSBayes(obj, thetahat, C, lvector, control=list(), ...)
```

Arguments

obj	The object from a regression model, for example, linear regression or Cox proportional-hazards regression. If obj is specified, then thetahat and C should be set to NULL.
thetahat	A vector of regression coefficients without the intercept. If thetahat is specified, then C should be provided as well, and obj should be set at NULL.
C	A variance covariance matrix of regression. If C is given, then thetahat should also be provided, and obj should be set at NULL.
lvector	A vector or a matrix that denotes linear combination of the parameters for which posterior estimates are desired. Note that, the order of the lvector should be as follows: the first parameter should always be the treatment indicator, then a set of binary covariates, and then the interactions between the treatment with covariates. See *Examples*.
control	A list of control parameters. See *Details*.
...	Additional arguments.

Details

The control argument is a list that can supply any of the following components:

tol A relative accuracy for numerical quadrature. Default is tol = 1.e-03.

epsilon A small positive quantity to ensure proper posterior resulting from Jeffreys' prior. Default is epsilon = 0.005.

ci Level of the credible interval. Default is ci = 0.95.

k A constant value to determine the interval width for searching the Bayesian credible interval, from lower to upper for a maximum of the density function. Default value for k is, k = qnorm((6+ci)/7) = 2.45.

transform = NULL, then no transformation is performed. If transform = "logit", which is at default, then logit transformation is applied for posterior density function to find the credibile interval, logit(x) = log(x/(1-x)).

print = TRUE or FALSE, indicating whether or not we want to print control parameters and progress. Default is FALSE.

Author(s)

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References

Dixon D. and Simon R. (1991). Bayesian Subset Analysis. *Biometrics*, 47, 871-881

Examples

```
# ex1 - use given thetahat and C matrix, and set "obj=NULL".
# an example from the clinical trial reported by Fisher(1988)
```

```
thetahat   <- c(-1.57,-0.52,-0.39,.68, 1.09, 0.68, 0.91)
names(thetahat) <- c("trt","Sex","Age","Stage","trt*sex","trt*age","trt*stage")
p <- length(thetahat)

C <- matrix(NA, p, p)
C[upper.tri(C, diag=TRUE)] <- c( .1502, .0141, .0505, .0198, .0042, .0506,
 .0389, -.0038, .0041, .0538, -.0361, -.0505, -.0042, .0039, .1037, -.0445,
 -.0042, -.0507, -.0041, -.0046, .1066,-.1209, .0037, -.0041, -.0536, -.0025,
 .0120, .1474)
C[lower.tri(C)] <- t(C)[lower.tri(t(C))]

# define lvector
trt  <- rep(1,8)
cov  <- as.data.frame(matrix(rep(0,24), ncol=3))
lmatrix<-as.matrix(cbind(trt,cov,rep(1:0,each=4),rep(rep(0:1,each=2),2), rep(0:1,4)))
dimnames(lmatrix)[[2]]<-c("trt","Sex","Age","Stage","trt*sex","trt*age","trt*stage")

lvector <- lmatrix[2,]    # for 1 subset
#> lvector
#      trt       Sex       Age     Stage   trt*sex   trt*age trt*stage
#        1         0         0         0         1         0         1
# treatment effect for the subset of Female under 65 at stage C.
# in this case the reference group is Male, under 65 years, at stage B.

#lvector <- lmatrix       # for all 8 subsets

result <- DSBayes(NULL, thetahat, C, lvector)


#############################################################################
# ex2 - use "obj" option, and set "thetahat=NULL" and "C=NULL"
# To run ex2, you need to remove hashmark(#).

#data(simsolvd)
#simsolvd$event <- 1-simsolvd$censor
#obj <- glm(event~trt*(age+beat+lvef+cardratio+sodium),
#                 family = "binomial", data = simsolvd)
#
#para    <- as.data.frame(matrix(rep(rep(0,5),5), ncol=5))
#lmatrix <- as.matrix(cbind(rep(1,5),para[1:5,],diag(1,5)))
#dimnames(lmatrix)[[2]] <- c("trt","age","beat","lvef","cardratio","sodium",
#"trt*age","trt*beat","trt*lvef","trt*cardratio","trt*sodium")

#lvector   <- lmatrix[2,]      # for 1 subset
#out <- DSBayes(obj, NULL, NULL, lvector)
```

---

simsolvd *Simulated SOLVD-Trial data set*

Description

A simulated clinical trial based on the design of the Studies of Left Ventricular Dysfunction Trial (SOLVD-T), a placebo-controlled trial of the angiotensin-converting-enzyme inhibitor enalapril for patients with congestive heart failure.

Usage

```
data(simsolvd)
```

Format

A data frame with 2569 observations on the following 12 variables.

trt indicator for enalapril group

age age at baseline (centered and scaled)

beat pulse at baseline (centered and scaled)

lymphocyte lymphocyte count at baseline (centered and scaled)

lvef left ventricular ejection fraction at baseline (centered and scaled)

noise simulated vector of random uniform variables

nyha indicator whether New York Heart Association score greater than 2

cardratio indicator whether cardiothoracic ratio is greater than 0.5

creatinine creatinine at baseline (centered and scaled)

sodium sodium at baseline (centered and scaled)

ttodthorchfhosp time to death or hospitalization in days

censor indicator whether censored (1) or an event (0)

current indicator whether current smoker

Source

Simulated data set based on the clinical study reported by: Yusuf, S. et al. (1991). Effect of Enalapril on Survival in Patients with Reduced Left-Ventricular Ejection Fractions and Congestive-Heart-Failure. *NEJM* 325:293-302.

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